SEQUENCE LISTING

<110> Kim, Tae-Wan
Lee, Hahn-Jun

<120> NOVEL MODULATORS OF AMYLOID-BETA PRODUCTION AND USES THEREOF

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<170> PatentIn version 3.1

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35 40 45

Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
50 55 60

Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65 70 75 80

Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95

Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110

Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115 120 125

Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
130 135 140

Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser

145 150 155 160

Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
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Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
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Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195 200 205

Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
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Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
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Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
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Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
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Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110

Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
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Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
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Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
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Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
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Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
180 185 190

Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195 200 205

Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
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Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
50 55 60

Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65 70 75 80

Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95

Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110

Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115 120 125

Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
130 135 140

Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
145 150 155 160

Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
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Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
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Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195 200 205

Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
210 215 220

Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
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Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
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Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
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Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95

Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110

Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115 120 125

Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
130 135 140

Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
145 150 155 160

Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
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Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
180 185 190

Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195 200 205

Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
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Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
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Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
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Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
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Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
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Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
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Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
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Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
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Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
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Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
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Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195 200 205

Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
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Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
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Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
180 185 190

Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
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210 215 220

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cgtttgtctc tgtctatatc cgagaaatgt tccgatttgc atattataaa ctcttaaaaa 300

aagccagtga aggtttgaag agtataaacc caggtgagac agcaccctct atgcgactgc 360

tggcctatgt ttctggcttg ggctttggaa tcatgagtgg agtattttcc tttgtgaata 420

ccctatctga ctccttgggg ccaggcacag tgggcattca tggagattct cctcaattct 480

tcctttattc agctttcatg acgctggtca ttatcttgct gcatgtattc tggggcattg 540

tatttttga tggctgtgag aagaaaaagt ggggcatcct ccttatcgtt ctcctgaccc 600

acctgctggt gtcagcccag accttcataa gttcttatta tggaataaac ctggcgtcag 660

catttataat cctggtgctc atgggcacct gggcattctt agctgcggga ggcagctgcc 720

gaagcctgaa actctgcctg ctctgccaag acaagaactt tcttctttac aaccagcgct 780

ccagataacc tcagggaacc agcacttccc aaaccgcaga ctacatcttt agaggaagca 840

caactgtgcc tttttctgaa aatccctttt tctggtggaa aaaaa 885

<210> 14

<211> 257

<212> PRT

<213> Homo sapiens

<400> 14

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly Pro
1 5 10 15

Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Thr Glu Pro Leu Arg Ile
20 25 30

Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Ile
35 40 45

Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile Asp Asn Lys Asp
50 55 60

Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly Ala Phe Val Ser Val
65 70 75 80

Tyr Ile Arg Glu Met Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95

Ala Ser Glu Gly Leu Lys Ser Ile Asn Pro Gly Glu Thr Ala Pro Ser
100 105 110

Met Arg Leu Leu Ala Tyr Val Ser Gly Leu Gly Phe Gly Ile Met Ser
115 120 125

Gly Val Phe Ser Phe Val Asn Thr Leu Ser Asp Ser Leu Gly Pro Gly
130 135 140

Thr Val Gly Ile His Gly Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala
145 150 155 160

Phe Met Thr Leu Val Ile Ile Leu Leu His Val Phe Trp Gly Ile Val
165 170 175

Phe Phe Asp Gly Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val
180 185 190

Leu Leu Thr His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr
195 200 205

Tyr Gly Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly
210 215 220

Thr Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
225 230 235 240

Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg Ser
245 250 255

Arg

<210> 15

<211> 762

<212> DNA

<213> Drosophila melanogaster

<400> 15

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ttcggaccgc ccttcgcctt gttcgtcttc accatcgcca atgatccagt gcggatcatc 120

attctgattg cggcggcatt cttctggctg ctttccctgc tgatctcttc cctgtggtat 180

gccctgattc cgctgaagga gttcctggca tttggcgtgg tcttctcggt gtgcttccag 240

gaagccttcc ggtacatcat ctaccggata ctgcgcagca cggagcaggg attgcacgcc 300

gtggcggagg acacgcgagt gacggacaac aagcacatcc tggcctatgt ctccggcttg 360

ggattcggca ttatatccgg gatgtttgca ctggtcaatg tgctggctga tatgagtggt 420

cccggcacca tgggcttgaa gggcggaact gagctattct tcgtcacctc ggctgcccag 480

gcgttgtcga ttatcctgct gcacaccttc tggagcgtta ttttcttcaa cgcattcgac 540

acaaacaact atatccacat aggctatgtg gttttcagcc acctgttcgt ctccctgata 600

actctgctca atgccaatga gctttacacg accactctgc tgataaacta cttggtcacc 660

atacttacgg gagtcctggc cttccgggtg gctggaggaa catctcgcag tttcagaaaa 720

ttcataacat gccagtaaac atactcctag tattaaccgc ct 762

<210> 16

<211> 238

<212> PRT

<213> Drosophila melanogaster

<400> 16

Met Thr Leu Pro Glu Phe Phe Gly Cys Thr Phe Ile Ala Phe Gly Pro
1 5 10 15

Pro Phe Ala Leu Phe Val Phe Thr Ile Ala Asn Asp Pro Val Arg Ile
20 25 30

Ile Ile Leu Ile Ala Ala Ala Phe Phe Trp Leu Leu Ser Leu Leu Ile
35 40 45

Ser Ser Leu Trp Tyr Ala Leu Ile Pro Leu Lys Glu Phe Leu Ala Phe
50 55 60

Gly Val Val Phe Ser Val Cys Phe Gln Glu Ala Phe Arg Tyr Ile Ile
65 70 75 80

Tyr Arg Ile Leu Arg Ser Thr Glu Gln Gly Leu His Ala Val Ala Glu
85 90 95

Asp Thr Arg Val Thr Asp Asn Lys His Ile Leu Ala Tyr Val Ser Gly
100 105 110

Leu Gly Phe Gly Ile Ile Ser Gly Met Phe Ala Leu Val Asn Val Leu
115 120 125

Ala Asp Met Ser Gly Pro Gly Thr Met Gly Leu Lys Gly Gly Thr Glu
130 135 140

Leu Phe Phe Val Thr Ser Ala Ala Gln Ala Leu Ser Ile Ile Leu Leu
145 150 155 160

His Thr Phe Trp Ser Val Ile Phe Phe Asn Ala Phe Asp Thr Asn Asn
165 170 175

Tyr Ile His Ile Gly Tyr Val Val Phe Ser His Leu Phe Val Ser Leu
180 185 190

Ile Thr Leu Leu Asn Ala Asn Glu Leu Tyr Thr Thr Thr Leu Leu Ile
195 200 205

Asn Tyr Leu Val Thr Ile Leu Thr Gly Val Leu Ala Phe Arg Val Ala
210 215 220

Gly Gly Thr Ser Arg Ser Phe Arg Lys Phe Ile Thr Cys Gln
225 230 235

<210> 17

<211> 2301

<212> DNA

<213> Homo sapiens

<400> 17

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gagggcccgg gagacgcggg agagcgtcga agagagaggt gcggaagggg ctggaggaac 180

tggggcaagc ctgggagcct gaattgggga cgataagtcg gaggtgaagt ttgggcggag 240

gtgaggggtt gggtctggga gatttgtcct ttcccgcagt tggtttccac cttccaagga 300

tctcacagat tcctcctata ttcctcccag cgacgtcaga gaaggcccaa ggccgagact 360

cgtgaggggg ctgtgctgac ctaggcaggc cgagtcaggt gccttagggg aggatccagg 420

aacggatacc tcgcccttcc gtgctcgcac actctggctg tcatcgctct gaagactctt 480

taattagatt tctccccttt ccagtgcgtt cacttttcta cagatgagtc tcttggtgga 540

gacagttacc ctacctggtc catgtctccc taaccatccg gaaggctaac ttccactttt 600

caagcagctt tggctggttt ccctccttga tttctctggc tcccactact attgcttgtc 660

tcactgcccc tgtcttttct cagggcattt ttctggctgg tctccctgct cctggcctct 720

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ctcctgattt ttggtgctgc tgtctctgtc cttctacagg aggtgttccg ctttgcctac 840

tacaagctgc ttaagtaaga agatggagtg gtctggaggg gagaggggca aaggactgca 900

ctatgggaag tggggcagcc cctgggtgct ggtttggaag aggaggcact aagggaggac 960

attagaggga aaggagcatc cctgccctcc ctcatgtttc ccctacccca ccccacccca 1020

ggaaggcaga tgaggggtta gcatcgctga gtgaggacgg aagatcaccc atctccatcc 1080

gccagatggc ctatggtgag ccaagggaga gggactggag gagggagttg gacagccccc 1140

tcctctaggg aagtctctaa atatccacat gttctaagtg gcttcttact ttccttcatc 1200

cgtcacttcc aaagaaagtt ggtctggagg gagagtagat gtgaaagaat tgtaaccggg 1260

aatggggagg ggtcagtggt gaacaggcaa tagtgtgatc tctgacattg atgagatcct 1320

cccttccccc agtttctggt ctctccttcg gtatcatcag tggtgtcttc tctgttatca 1380

atattttggc tgatgcactt gggccaggtg tggttgggat ccatggagac tcaccctatt 1440

acttcctgac ttcaggtaag atccaccttc tatctagcct ttacccccca tccatccttg 1500

tccctgatct gatttattgg ccttccctga gagacttctt tggctcaaca tctcaggagc 1560

ctgggagaag atcagggatg tatctcctcc ccatctccct ccctgcagcc tttctgacag 1620

cagccattat cctgctccat acctttttggg gagttgtgtt ctttgatgcc tgtgagagga 1680

gacggtactg ggctttgggc ctggtggttg ggagtcacct actgacatcg ggactggtga 1740

gttggagaca ggggcctgag ttagggagaa aagcatttaa tggtgagtgg gatgtggggg 1800

aaagggtatc ctcacttctt aacatttttа acttacctgg gaggaggagg aaaggtgagt 1860

ctttcaaggt ctctcacctc agcatcattt ctatcacctg ctctggggag gaggttgaaa 1920

ggattagtca aactgtaatg cagagggcct gaggtgagca ggagcggcag aaacctttga 1980

gtttctgagg agctgaaaat caaaagtccc cttaaccaca agatgttggt gctctgaagg 2040

gaaagactgg agaatttgag agagatatct gggagtcaga aaggtacaga gagaatatgg 2100

ggattaggtc gagggagaat ctaatctctt tcctactctt accctccttc ctagacattc 2160

ctgaacccct ggtatgaggc cagcctgctg cccatctatg cagtcactgt ttccatgggg 2220

ctctgggcct tcatcacagc tggagggtcc ctccgaagta ttcagcgcag cctcttgtgt 2280

aaggactgac tacctggact g 2301

<210> 18

<211> 1200

<212> PRT

<213> Mus musculus

<400> 18

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Gly Cys Thr Gly Cys Cys Cys Ala Gly Thr Cys Ala Thr Gly Gly Gly
20 25 30

Gly Gly Cys Thr Gly Cys Thr Gly Thr Gly Thr Thr Thr Thr Thr Cys
35 40 45

Gly Gly Ala Thr Gly Cys Ala Cys Cys Thr Thr Cys Gly Thr Cys Gly

50 55 60

Cys Gly Thr Thr Cys Gly Gly Cys Cys Cys Ala Gly Cys Cys Thr Thr
65 70 75 80

Cys Thr Cys Cys Cys Thr Thr Thr Thr Cys Cys Thr Gly Ala Thr Cys
85 90 95

Ala Cys Thr Gly Thr Ala Gly Cys Thr Gly Gly Ala Gly Ala Cys Cys
100 105 110

Cys Ala Cys Thr Thr Cys Gly Gly Gly Thr Thr Ala Thr Cys Ala Thr
115 120 125

Cys Cys Thr Gly Gly Thr Gly Gly Cys Gly Gly Gly Ala Gly Cys Cys
130 135 140

Thr Thr Thr Thr Thr Cys Thr Gly Gly Cys Thr Gly Gly Thr Cys Thr
145 150 155 160

Cys Cys Cys Thr Gly Cys Thr Cys Thr Thr Gly Gly Cys Thr Thr Cys
165 170 175

Thr Gly Thr Gly Gly Thr Cys Thr Gly Gly Thr Thr Cys Ala Thr Cys
180 185 190

Thr Thr Gly Gly Thr Cys Cys Ala Thr Gly Thr Gly Ala Cys Ala Gly
195 200 205

Ala Cys Cys Gly Ala Thr Cys Ala Gly Ala Thr Gly Cys Ala Cys Gly
210 215 220

Gly Cys Thr Cys Cys Ala Gly Thr Ala Thr Gly Gly Cys Cys Thr Cys

225 230 235 240

Cys Thr Gly Ala Thr Thr Thr Thr Thr Gly Gly Thr Gly Cys Thr Gly
245 250 255

Cys Thr Gly Thr Cys Thr Cys Thr Gly Thr Cys Cys Thr Thr Cys Thr
260 265 270

Ala Cys Ala Gly Gly Ala Ala Gly Thr Gly Thr Thr Cys Cys Gly Thr
275 280 285

Thr Thr Thr Gly Cys Thr Thr Ala Cys Thr Ala Cys Ala Ala Gly Cys
290 295 300

Thr Cys Cys Thr Thr Ala Ala Gly Ala Ala Gly Gly Cys Ala Gly Ala
305 310 315 320

Thr Gly Ala Gly Gly Gly Cys Thr Thr Ala Gly Cys Ala Thr Cys Ala
325 330 335

Cys Thr Gly Ala Gly Thr Gly Ala Gly Gly Ala Cys Gly Gly Ala Ala
340 345 350

Gly Ala Thr Cys Ala Cys Cys Cys Ala Thr Cys Thr Cys Cys Ala Thr
355 360 365

Cys Cys Gly Ala Cys Ala Gly Ala Thr Gly Gly Cys Cys Thr Ala Thr
370 375 380

Gly Thr Thr Thr Cys Thr Gly Gly Thr Cys Thr Gly Thr Cys Cys Thr
385 390 395 400

Thr Cys Gly Gly Thr Ala Thr Cys Ala Thr Cys Ala Gly Thr Gly Gly
405 410 415

Thr Gly Thr Cys Thr Thr Cys Thr Cys Thr Gly Thr Thr Ala Thr Cys
420 425 430

Ala Ala Thr Ala Thr Thr Thr Thr Gly Gly Cys Thr Gly Ala Thr Gly
435 440 445

Cys Ala Cys Thr Thr Gly Gly Gly Cys Cys Ala Gly Gly Thr Gly Thr
450 455 460

Gly Gly Thr Thr Gly Gly Gly Ala Thr Cys Cys Ala Thr Gly Gly Ala
465 470 475 480

Gly Ala Cys Thr Cys Ala Cys Cys Cys Thr Ala Thr Thr Ala Cys Thr
485 490 495

Thr Cys Cys Thr Gly Ala Cys Thr Thr Cys Ala Gly Cys Cys Thr Thr
500 505 510

Thr Cys Thr Gly Ala Cys Ala Gly Cys Ala Gly Cys Cys Ala Thr Thr
515 520 525

Ala Thr Cys Cys Thr Gly Cys Thr Cys Cys Ala Cys Ala Cys Cys Thr
530 535 540

Thr Thr Thr Gly Gly Gly Gly Ala Gly Thr Thr Gly Thr Gly Thr Thr
545 550 555 560

Cys Thr Thr Thr Gly Ala Thr Gly Cys Cys Thr Gly Thr Gly Ala Gly
565 570 575

Ala Gly Gly Ala Gly Ala Cys Gly Gly Thr Ala Cys Thr Gly Gly Gly
580 585 590

Cys Thr Thr Thr Gly Gly Gly Cys Cys Thr Gly Gly Thr Ala Gly Thr
595 600 605

Thr Gly Gly Gly Ala Gly Thr Cys Ala Cys Cys Thr Thr Cys Thr Gly
610 615 620

Ala Cys Ala Thr Cys Gly Gly Gly Ala Cys Thr Gly Ala Cys Ala Thr
625 630 635 640

Thr Cys Cys Thr Gly Ala Ala Cys Cys Cys Cys Thr Gly Gly Thr Ala
645 650 655

Thr Gly Ala Gly Gly Cys Thr Ala Gly Cys Cys Thr Gly Cys Thr Gly
660 665 670

Cys Cys Cys Ala Thr Cys Thr Ala Thr Gly Cys Ala Gly Thr Cys Ala
675 680 685

Cys Cys Gly Thr Thr Thr Cys Cys Ala Thr Gly Gly Gly Gly Cys Thr
690 695 700

Cys Thr Gly Gly Gly Cys Gly Thr Thr Cys Ala Thr Cys Ala Cys Ala
705 710 715 720

Gly Cys Cys Gly Gly Ala Gly Gly Cys Thr Cys Cys Cys Thr Cys Cys
725 730 735

Gly Ala Ala Gly Thr Ala Thr Cys Cys Ala Gly Cys Gly Cys Ala Gly
740 745 750

Cys Cys Thr Thr Thr Cys Gly Thr Gly Thr Ala Ala Gly Gly Ala Cys
755 760 765

Thr Gly Ala Cys Thr Ala Cys Cys Thr Gly Gly Ala Cys Thr Gly Ala
770 775 780

Thr Cys Gly Cys Cys Cys Gly Ala Cys Ala Gly Ala Thr Cys Cys Cys
785 790 795 800

Ala Thr Cys Thr Gly Cys Cys Thr Ala Thr Cys Cys Ala Cys Thr Gly
805 810 815

Cys Cys Cys Ala Thr Gly Ala Cys Thr Gly Ala Ala Cys Cys Cys Ala
820 825 830

Gly Cys Cys Cys Cys Ala Gly Cys Cys Cys Gly Gly Gly Thr Cys Cys
835 840 845

Ala Thr Thr Gly Cys Cys Cys Thr Cys Ala Thr Cys Cys Thr Cys Cys
850 855 860

Gly Thr Cys Thr Cys Cys Thr Cys Gly Cys Thr Gly Ala Thr Gly Thr
865 870 875 880

Gly Cys Cys Cys Cys Gly Cys Thr Thr Cys Cys Thr Thr Cys Cys Gly
885 890 895

Gly Gly Thr Thr Thr Gly Gly Cys Gly Thr Thr Gly Thr Cys Cys Ala
900 905 910

Thr Thr Thr Gly Thr Gly Ala Cys Cys Thr Gly Thr Ala Gly Thr Cys
915 920 925

Thr Cys Thr Ala Ala Gly Cys Thr Thr Thr Cys Thr Cys Ala Gly Gly
930 935 940

Ala Gly Cys Ala Gly Cys Cys Thr Gly Gly Gly Thr Gly Cys Ala Gly
945 950 955 960

Cys Cys Ala Gly Thr Cys Ala Gly Gly Gly Ala Cys Thr Gly Gly Thr
965 970 975

Gly Gly Gly Thr Thr Thr Gly Ala Ala Thr Cys Thr Gly Cys Ala Thr
980 985 990

Cys Thr Cys Thr Cys Cys Cys Cys Ala Cys Cys Ala Cys Cys Thr Gly
995 1000 1005

Gly Gly Gly Ala Cys Cys Cys Cys Cys Thr Thr Gly Thr Thr Gly
1010 1015 1020

Thr Cys Cys Ala Gly Gly Thr Cys Thr Cys Cys Cys Cys Ala Thr
1025 1030 1035

Gly Thr Gly Thr Cys Ala Gly Thr Gly Cys Thr Cys Cys Ala Cys
1040 1045 1050

Cys Cys Thr Cys Ala Cys Cys Cys Thr Gly Cys Cys Cys Ala Thr
1055 1060 1065

Gly Ala Cys Thr Cys Ala Cys Cys Cys Cys Gly Cys Thr Thr Cys
1070 1075 1080

Cys Cys Cys Thr Cys Thr Gly Cys Ala Gly Gly Cys Cys Gly Cys

1085 1090 1095

Cys Gly Gly Cys Ala Gly Gly Ala Gly Gly Ala Cys Ala Gly Thr
1100 1105 1110

Cys Gly Gly Gly Thr Gly Ala Thr Gly Gly Thr Gly Thr Ala Cys
1115 1120 1125

Thr Cys Thr Gly Cys Cys Cys Thr Gly Cys Gly Cys Ala Thr Cys
1130 1135 1140

Cys Cys Ala Cys Cys Cys Gly Ala Gly Gly Ala Cys Thr Gly Ala
1145 1150 1155

Gly Gly Gly Ala Ala Cys Ala Thr Gly Gly Gly Gly Gly Gly Gly
1160 1165 1170

Cys Cys Cys Cys Thr Gly Gly Gly Cys Cys Thr Gly Gly Gly Gly
1175 1180 1185

Thr Gly Cys Cys Cys Thr Cys Cys Cys Gly Ala Thr
1190 1195 1200

<210> 19

<211> 247

<212> PRT

<213> Mus musculus

<400> 19

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro
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Ala Phe Ser Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val
20 25 30

Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
35 40 45

Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
50 55 60

Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65 70 75 80

Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95

Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110

Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115 120 125

Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
130 135 140

Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
145 150 155 160

Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
165 170 175

Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
180 185 190

Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195 200 205

Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
210 215 220

Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
225 230 235 240

Arg Ser Leu Ser Cys Lys Asp
245

<210> 20

<211> 867

<212> DNA

<213> Mus musculus

<400> 20

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gttatcatcc tggtggcggg agccttttc tggctggtct ccctgctctt ggcttctgtg 180

gtctggttca tcttggtcca tgtgacagac cgatcagatg cacggctcca gtatggcctc 240

ctgatttttg gtgctgctgt ctctgtcctt ctacaggaag tgttccgttt tgcttactac 300

aagctcctta agaaggcaga tgagggctta gcatcactga gtgaggacgg aagatcaccc 360

atctccatcc gacagatggc ctatgtttct ggtctgtcct tcggtatcat cagtggtgtc 420

ttctctgtta tcaatatttt ggctgatgca cttgggccag gtgtggttgg gatccatgga 480

gactcaccct attacttcct gacttcagcc tttctgacag cagccattat cctgctccac 540

acctttggg gagttgtgtt ctttgatgcc tgtgagagga gacggtactg ggctttgggc 600

ctggtagttg ggagtcacct tctgacatcg ggactgacat tcctgaaccc ctggtatgag 660

gctagcctgc tgcccatcta tgcagtcacc gtttccatgg ggctctgggc gttcatcaca 720

gccggaggct ccctccgaag tatccagcgc agcctttcgt gccgccggca ggaggacagt 780

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cccctgggcc tggggtgccc tcccgat 867

<210> 21

<211> 265

<212> PRT

<213> Mus musculus

<400> 21

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro
1 5 10 15

Ala Phe Ser Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val
20 25 30

Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
35 40 45

Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
50 55 60

Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65 70 75 80

Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95

Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100 105 110

Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115 120 125

Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
130 135 140

Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
145 150 155 160

Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
165 170 175

Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
180 185 190

Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195 200 205

Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
210 215 220

Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
225 230 235 240

Arg Ser Leu Ser Cys Arg Arg Gln Glu Asp Ser Arg Val Met Val Tyr
245 250 255

Ser Ala Leu Arg Ile Pro Pro Glu Asp
260 265

<210> 22

<211> 92

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(92)

<223> PCR primer

<400> 22

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ctcggggatg cagaattccg acatgactca gg 92

<210> 23

<211> 77

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(77)

<223> PCR primer

<400> 23

gccgactcta gactagaggc ttgcataatc tggcacatca tatggatagt tctgcatctg 60

ctcaaagaac ttgtagg 77

<210> 24

<211> 41

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(41)

<223> PCR primer

<400> 24

cccgggggta cctcttcgat ggaaatgcgt ctgaatgcgg c 41

<210> 25

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(36)

<223> PCR primer

<400> 25

aaatttgaat tcaccaaata atgcggcatt gcttgc 36

<210> 26

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(30)

<223> PCR primer

<400> 26

gccatggggg ctgcggtgtt tttcggctgc 30

<210> 27

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(27)

<223> PCR primer

<400> 27

gtccaggtag tcagtcctta cacaagagct gc 32

<210> 28

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(32)

<223> PCR primer

<400> 28

gtccttacac aagaggctgc gctgaatact tc 32

<210> 29

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(31)

<223> PCR primer

<400> 29

gtcctcgggt gggatgcgca gggcagaata c 31

<210> 30

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(27)

<223> PCR primer

<400> 30

gaattaatac gactcactat agggaga 27

<210> 31

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(23)

<223> PCR primer

<400> 31

atttaggtga cactatagaa gcg 23

<210> 32

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(31)

<223> PCR primer

<400> 32

gggctcgcct ctgaggatga cgccaatgtg g 31

<210> 33

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(32)

<223> PCR primer

<400> 33

aatgcggagg ggtcctcttg gcgaaaggac ag 32

<210> 34

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(34)

<223> PCR primer

<400> 34

atggaaatgc gtctgaatgc ggcttccata tggc 34

<210> 35

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(31)

<223> PCR primer

<400> 35

ttcgtatgga ctgtctccaa agttgtttcc g 31

<210> 36

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(33)

<223> PCR primer

<400> 36

gatgcagaat ccgacatgac tcaggatatg aag 33

<210> 37

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(33)

<223> PCR primer

<400> 37

gttctgcatc tgctcaaaga acttgtaggt tgg 33

<210> 38

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(29)

<223> PCR primer

<400> 38

cacattggcc aagctggtgt ccagatcgg 29

<210> 39

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(28)

<223> PCR primer

<400> 39

gcgcaacgag gccgtaatgg aggaaacg 28

<210> 40

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(30)

<223> PCR primer

<400> 40

cagctgaaac gaacctttct tggcttcgac 30

<210> 41

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(30)

<223> PCR primer

<400> 41

caaatcgggt gcacaaacat ttaggcattc 30

<210> 42

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(31)

<223> PCR primer

<400> 42

gctatgtcgc tatcaagcct gctgcccacg c 31

<210> 43

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(34)

<223> PCR primer

<400> 43

gaatgtactg ggcgggaccc gccttctggg catg 34

<210> 44

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(34)

<223> PCR primer

<400> 44

cggatgctga cgacgtcttc aagcacaatg cttg 34

<210> 45

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(34)

<223> PCR primer

<400> 45

ccaggtcgta tcgtccgtag tcgcggaaga ggag 34

<210> 46

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(34)

<223> PCR primer

<400> 46

ttaaatatgt ctgacaacaa cagcggatcc ggag 34

<210> 47

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(35)

<223> PCR primer

<400> 47

ttaacataac gctcatagaa ctccagcgaa ctaac 35

<210> 48

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(26)

<223> PCR primer

<400> 48

ccggaaatat catcatttca ggcagc 26

<210> 49

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(27)

<223> PCR primer

<400> 49

gtcgaggacc attagctttg tttcctc 27

<210> 50

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(28)

<223> PCR primer

<400> 50

tcgcataata atcaatacaa tccacctg 28

<210> 51

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(27)

<223> PCR primer

<400> 51

gatgccgcca ctcttgaaga tggccag 27

<210> 52

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(34)

<223> PCR primer

<400> 52

gatgacgttg cccgagttct ttggctgcac cttc 34

<210> 53

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(32)

<223> PCR primer

<400> 53

aatactagga gtatgtttac tggcatgtta tg 32

<210> 54

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(23)

<223> PCR primer

<400> 54

taatacgact cactataggg aga 23

<210> 55

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(23)

<223> PCR primer

<400> 55

atttaggtga cactatagaa gcg 23

<210> 56

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> sense RNA

<400> 56

gccaucauga ucagugucau uaa 23

<210> 57

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> antisense RNA

<400> 57

aaugacacug aucaugaugg cug 23

<210> 58

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> sense RNA

<400> 58

cacccucauc augaucagcg uaa 23

<210> 59

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> antisense RNA

<400> 59

acgcugauca ugaugagggu gug 23

<210> 60

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> sense RNA

<400> 60

ccugcucaac gccacucauc aaa 23

<210> 61

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> antisense RNA

<400> 61

ugaugagugg cguugagcag gug 23

<210> 62

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> sense RNA

<400> 62

uagaugaggg caugcagauc caa 23

<210> 63

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> antisense RNA

<400> 63

ggaucugcau gcccucaucu aug 23

<210> 64

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> sense RNA

<400> 64

cggcugcacu uucgucgcgu uaa 23

<210> 65

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> antisense RNA

<400> 65

aacgcgacga aagugcagcc gug 23

<210> 66

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> sense RNA

<400> 66

cgucccuugu uugguucaug gaa 23

<210> 67

<211> 23

<212> RNA

<213> Artificial sequence

<220>

<221> misc_RNA

<222> (1)..(23)

<223> antisense RNA

<400> 67

ccaugaacca aacaagggac gug 23

<210> 68

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(30)

<223> PCR primer

<400> 68

ccacccccct tcccacctga ccagccatgg 30

<210> 69

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<221> primer_bind

<222> (1)..(30)

<223> PCR primer

<400> 69

cactgtccag aactggagat ggagaaatac 30

<210> 70

<211> 258

<212> PRT

<213> Mus musculus

<400> 70

Met Thr Leu Pro Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly Pro
1 5 10 15

Ala Phe Ala Leu Tyr Leu Phe Thr Ile Ala Thr Asp Pro Leu Arg Val
20 25 30

Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
35 40 45

Ser Ser Met Phe Trp Phe Leu Val Arg Val Ile Thr Asn Asn Arg Asp
50 55 60

Glu Ser Val Gln Asn Tyr Leu Leu Ile Phe Gly Ala Leu Leu Ser Val
65 70 75 80

Cys Ile Gln Glu Leu Phe Arg Leu Ala Tyr Tyr Lys Leu Leu Lys Lys
85 90 95

Ala Ser Glu Gly Leu Lys Ser Ile Asn Pro Glu Glu Asp Ile Ala Pro
100 105 110

Ser Met Arg Leu Leu Ala Tyr Val Ser Gly Leu Gly Phe Gly Ile Met
115 120 125

Ser Gly Val Phe Ser Phe Val Asn Thr Leu Ser Asn Ser Leu Gly Pro
130 135 140

Gly Thr Val Gly Ile His Gly Asp Ser Pro Gln Phe Phe Leu Asn Ser
145 150 155 160

Ala Phe Met Thr Leu Val Val Ile Met Leu His Val Phe Trp Gly Val
165 170 175

Val Phe Phe Asp Gly Cys Glu Lys Asn Lys Trp Tyr Thr Leu Leu Thr
180 185 190

Val Leu Leu Thr His Leu Val Val Ser Thr Gln Thr Phe Leu Ser Pro
195 200 205

Tyr Tyr Glu Val Asn Leu Val Thr Ala Tyr Ile Ile Met Val Leu Met
210 215 220

Gly Ile Trp Ala Phe Tyr Val Ala Gly Gly Ser Cys Arg Ser Leu Lys
225 230 235 240

Phe Cys Leu Leu Cys Gln Asp Lys Asp Phe Leu Leu Tyr Asn Gln Arg
245 250 255

Ser Arg

<210> 71

<211> 2563

<212> DNA

<213> Drosophila melanogaster

<400> 71

ggccggctgc cttgcctttc gaaagtcagt tgcgtgcgag ccgcgagcgc gagatcatca 60

aactgagaaa gtcggactgc gactcgaaac tgaaattgaa actgaaagag agaaatattc 120

aaattgtcgt gtgtgtgggt gcaagcagag aatatatatc tcaagaatat ctgaatacaa 180

gctcctggat ttacgagcag caaaactaag ttaccaatgt gcgagccgaa aaaagcgagt 240

gaaaaacgtg cgaatatgcc aactaactaa agacatttgg attacaagaa acccacgcat 300

tttggattat aaacattgcg acaggcagaa aaacctaaga atttcttcaa cggcgccagc 360

atggagaacc caacgcagaa tgtaaacgaa accaaggtgg atttgggcca ggagaaggag 420

aaggaggcgt cgcaggagga ggagcatgcc accgccgtca aggagaccat cattgacatt 480

cccgccgcgt gctccacttc ctccaactcc tcgtcgtacg acaccgattg cagcacggcg 540

agcagcacct gctgcacccg ccaaggcgag cacatctaca tgcaacgcga ggccatcccg 600

gccacgccac ttccggagtc ggaggatatc ggcctgctga agtacgtcca ccgccagcac 660

tggccctggt tcatcctagt gatctccatc attgagattg ccatcttcgc ctacgaccgc 720

tacacaatgc ccgcccagaa tttcgggcta cccgttccga ttccgtcgga ttcggtgctg 780

gtctatcggc cggaccggcg tctgcaggtg tggcgcttct ttagctacat gttcctgcac 840

gccaactggt tccacctggg cttcaatatc gtcatccagc tgttcttcgg cattcccctg 900

gaggtgatgc acggcacggc caggatcggc gtgatctaca tggcgggcgt ttttgccgga 960

tccctgggca ccagtgtcgt cgactcggag gtcttcctgg tgggcgccag cggtggcgtc 1020

tatgccctgt tggccgcaca tctggccaac atcacattga actatgcgca catgaagagc 1080

gcatccacgc aactcggatc agttgtcatc tttgtctcct gcgatctggg ctatgctctc 1140

tacacccaat acttcgatgg aagcgccttc gccaagggtc cccaggtgtc gtacattgcc 1200

cacctgacgg gagccctggc aggactaacg atcggcttcc tggtgctgaa gaacttcggt 1260

catcgggagt acgagcagct catctggtgg ctagcgttgg gcgtctactg tgccttcacc 1320

gtcttcgcca tcgttttcaa cctgatcaac acggtgaccg cccagctgat ggaggagcag 1380

ggtgaggtga ttacccagca tctgttgcac gacctgggag tgtcctaagt gtgaggttcg 1440

gagtcgtcag catgctcgca gggattcgga atctgcttga gcttcaggag agatcgagag 1500

acagagagtt ggtggaaaag aaaagttcac tcaacgattt agttcaaaac taattcgata 1560

ttcgtttggc ttttgctttt cgttagcatt atctcgttat cgttaccgtt tgcagttaaa 1620

cgtttcagtt gcgaaacata gtacacaaac tcataaaaaa aaaaacaaat caagagaaat 1680

acactggaca aaaaaaagag cgaggagtga ggagaacata aaccgaagcc gaaacgtgta 1740

aacaaatgtt gtgatagaac caaagactga atttatttcg cgtgtaaaaa ccaagtaaaa 1800

atcaagagga aaatcaaaga ggagaaacag aactaatcgc ctctcgctat gatttaaatg 1860

aacccaatta tccatgtttt caattaatgg tttgtctgtt ttcttaaatt atgtatttat 1920

tggccgcaat tactacgaat gaatcgaatc gaagcatcag caaactgtat caaattgttt 1980

atacatccat aagcataatg tgctccgaat tgtaggatta gtgttataat ttatatatat 2040

ttaggtataa ctagccctcc taacaaattg tttcaaattg taaatactat taagtcgcac 2100

actagtcaaa caacaacaac agcaacagca aaaacaacaa aaaatgtatg gaaaaccaca 2160

gcaaagaacc attcaattca gatcaattaa gcaaatcgag ttaaattaaa ttaaattata 2220

ctaaagtcac ttaatgcgtt acaaaatcga gcaaatattt atcgtaatcc ctacacacac 2280

acacacacac actcgaaagt attactaatt atatttattt atggtagggc agcgagggtt 2340

tattaattcg tcaattgagc gaactattta tttatttatt tatttaataa tttagtgaaa 2400

ttcacacaaa caagcacgaa aaaacaacaa caacacaaga gagagaagaa acaaaccaat 2460

tcaactgtaa aaatatccaa ttgaaaaata cacacgaaaa gccaaagaaa ataaaaaatc 2520

aaaacatttc aagaatacaa cagtaataac aaaatacaaa aaa 2563

<210> 72

<211> 355

<212> PRT

<213> Drosophila melanogaster

<400> 72

Met Glu Asn Pro Thr Gln Asn Val Asn Glu Thr Lys Val Asp Leu Gly
1 5 10 15

Gln Glu Lys Glu Lys Glu Ala Ser Gln Glu Glu Glu His Ala Thr Ala
20 25 30

Val Lys Glu Thr Ile Ile Asp Ile Pro Ala Ala Cys Ser Thr Ser Ser
35 40 45

Asn Ser Ser Ser Tyr Asp Thr Asp Cys Ser Thr Ala Ser Ser Thr Cys
50 55 60

Cys Thr Arg Gln Gly Glu His Ile Tyr Met Gln Arg Glu Ala Ile Pro
65 70 75 80

Ala Thr Thr Leu Pro Glu Ser Glu Asp Ile Gly Leu Leu Lys Tyr Val
85 90 95

His Arg Gln His Trp Pro Trp Phe Ile Leu Val Ile Ser Ile Ile Glu
100 105 110

Ile Ala Ile Phe Ala Tyr Asp Arg Tyr Thr Met Pro Ala Gln Asn Phe

115 120 125

Gly Leu Pro Val Pro Ile Pro Ser Asp Ser Val Leu Val Tyr Arg Pro
130 135 140

Asp Arg Arg Leu Gln Val Trp Arg Phe Phe Ser Tyr Met Phe Leu His
145 150 155 160

Ala Asn Trp Phe His Leu Gly Phe Asn Ile Val Ile Gln Leu Phe Phe
165 170 175

Gly Ile Pro Leu Glu Val Met His Gly Thr Ala Arg Ile Gly Val Ile
180 185 190

Tyr Met Ala Gly Val Phe Ala Gly Ser Leu Gly Thr Ser Val Val Asp
195 200 205

Ser Glu Val Phe Leu Val Gly Ala Ser Gly Gly Val Tyr Ala Leu Leu
210 215 220

Ala Ala His Leu Ala Asn Ile Thr Leu Asn Tyr Ala His Met Lys Ser
225 230 235 240

Ala Ser Thr Gln Leu Gly Ser Val Val Ile Phe Val Ser Cys Asp Leu
245 250 255

Gly Tyr Ala Leu Tyr Thr Gln Tyr Phe Asp Gly Ser Ala Phe Ala Lys
260 265 270

Gly Pro Gln Val Ser Tyr Ile Ala His Leu Thr Gly Ala Leu Ala Gly
275 280 285

Leu Thr Ile Gly Phe Leu Val Leu Lys Asn Phe Gly His Arg Glu Tyr

290 295 300

Glu Gln Leu Ile Trp Trp Leu Ala Leu Gly Val Tyr Cys Ala Phe Thr
305 310 315 320

Val Phe Ala Ile Val Phe Asn Leu Ile Asn Thr Val Thr Ala Gln Leu
325 330 335

Met Glu Glu Gln Gly Glu Val Ile Thr Gln His Leu Leu His Asp Leu
340 345 350

Gly Val Ser
355

<210> 73

<211> 1121

<212> DNA

<213> Drosophila melanogaster

<400> 73

ccagaaagca aaatagaaac aaattttcca tatttcatgc taaattggca cagatccgta 60

ctactatgct catgagtcga gcgctttgcc ggagctggct accccaggtg gcccgcagat 120

gtcatgctaa tgtgaatgtg ccaatcctgc ggataaactc tggtcatccg gcggcgaggt 180

catgtcggca gattcacagc aaccgaaaac agagcagcaa cctgaagccg acgactgggg 240

agcctgcggc agcggagcag aacaccccgg tgccggtgaa caatgtgatc aaggcggtgg 300

ccttcacggg agcatttacg gtcggctgct ttgcgggtgc caccatcctg gagtacgaga 360

acacacgtag cctaatccta gaaaaggctc gccaggcgag attcggttgg tggcagagtc 420

gttcgctggc ggacagggat tactggacac agatcaaaca agacatccgg cggcactggg 480

actcactgac acccggcgac aagatgtttg ctcctatctt actctgcaat ttggtggcct 540

tcgccatgtg gcgggtgccc gctctgaaat ccacaatgat tacctacttc acatccaatc 600

cagcggcgaa agtcgtctgc tggcccatgt tcctgtccac attcagccat tactcggcta 660

tgcacctttt cgccaatatg tacgtgatgc acagctttgc caacgctgcg gctgtatcgt 720

tgggtaaaga gcaattctta gcggtctacc tcagcgccgg cgtcttctcc agtctgatga 780

gcgtgctcta caaggcggcc acgagtcagg cggggatgtc cctgggtgcg tctggagcta 840

taatgacact gctggcctat gtatgcaccc agtatccgga cacacaactt agcattctct 900

ttctacccgc gttgacattc tccgctggag ctggtattaa agtgctaatg ggcatcgact 960

ttgctggcgt cgtgatgggc tggaagttct tcgatcacgc agcgcatttg ggcggcgcca 1020

tgtttggcat cttttgggcc acgtatgggg cacagatatg ggcaaagcgc attggtctac 1080

tgaattacta ccatgacctg cgccggacga agcagaaata g 1121

<210> 74

<211> 351

<212> PRT

<213> Drosophila melanogaster

<400> 74

Met Leu Met Ser Arg Ala Leu Cys Arg Ser Trp Leu Pro Gln Val Ala
1 5 10 15

Arg Arg Cys His Ala Asn Val Asn Val Pro Ile Leu Arg Ile Asn Ser
20 25 30

Gly His Pro Ala Ala Arg Ser Cys Arg Gln Ile His Ser Asn Arg Lys

35 40 45

Gln Ser Ser Asn Leu Lys Pro Thr Thr Gly Glu Pro Ala Ala Ala Glu
50 55 60

Gln Asn Thr Pro Val Pro Val Asn Asn Val Ile Lys Ala Val Ala Phe
65 70 75 80

Thr Gly Ala Phe Thr Val Gly Cys Phe Ala Gly Ala Thr Ile Leu Glu
85 90 95

Tyr Glu Asn Thr Arg Ser Leu Ile Leu Glu Lys Ala Arg Gln Ala Arg
100 105 110

Phe Gly Trp Trp Gln Ser Arg Ser Leu Ala Asp Arg Asp Tyr Trp Thr
115 120 125

Gln Ile Lys Gln Asp Ile Arg Arg His Trp Asp Ser Leu Thr Pro Gly
130 135 140

Asp Lys Met Phe Ala Pro Ile Leu Leu Cys Asn Leu Val Ala Phe Ala
145 150 155 160

Met Trp Arg Val Pro Ala Leu Lys Ser Thr Met Ile Thr Tyr Phe Thr
165 170 175

Ser Asn Pro Ala Ala Lys Val Val Cys Trp Pro Met Phe Leu Ser Thr
180 185 190

Phe Ser His Tyr Ser Ala Met His Leu Phe Ala Asn Met Tyr Val Met
195 200 205

His Ser Phe Ala Asn Ala Ala Ala Val Ser Leu Gly Lys Glu Gln Phe

210 215 220

Leu Ala Val Tyr Leu Ser Ala Gly Val Phe Ser Ser Leu Met Ser Val
225 230 235 240

Leu Tyr Lys Ala Ala Thr Ser Gln Ala Gly Met Ser Leu Gly Ala Ser
245 250 255

Gly Ala Ile Met Thr Leu Leu Ala Tyr Val Cys Thr Gln Tyr Pro Asp
260 265 270

Thr Gln Leu Ser Ile Leu Phe Leu Pro Ala Leu Thr Phe Ser Ala Gly
275 280 285

Ala Gly Ile Lys Val Leu Met Gly Ile Asp Phe Ala Gly Val Val Met
290 295 300

Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly Ala Met Phe
305 310 315 320

Gly Ile Phe Trp Ala Thr Tyr Gly Ala Gln Ile Trp Ala Lys Arg Ile
325 330 335

Gly Leu Leu Asn Tyr Tyr His Asp Leu Arg Arg Thr Lys Gln Lys
340 345 350